SEQUENCE LISTING

<110> Jung, Rudolf
     Beach, Larry R.
     Dress, Virginia M.
     Rao, A. Gururaj
     Ranch, Jerome P.
     Ertl, David S.
     Higgins, Regina K.

<120> Alteration of Amino Acid Compositions in
     Seeds

<130> 0815A

<150> US 09/020,716
<151> 1998-02-09

<160> 22

<170> FastSEQ for Windows Version 3.0

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     nucleotide 3361 to nucleotide 2947.

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2

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      expression vector. Zea mays promoter from
      nucleotide 676 to nucleotide 2198.

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4

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            <212> DNA
            <213> Artificial Sequence

            <220>
            <223> Modified gene based on Hordeum vulgare from
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                  expression vector.  Zea mays promoter from
                  nucleotide 3271 to nucleotide 1834.

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gcgatgattg agtaataatg tgtcacgcat caccatgcat gggtggcagt ctcagtgtga   2820
gcaatgacct gaatgaacaa ttgaaatgaa aagaaaaaag tattgttcca aattaaacgt   2880
tttaaccttt taataggttt atacaataat tgatatatgt tttctgtata tgtctaattt   2940
gttatcatcc atttagatat agacgaaaaa aaatctaaga actaaaacaa atgctaattt   3000
gaaatgaagg gagtatatat tgggataatg tcgatgagat ccctcgtaat atcaccgaca   3060
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ggcccggtac ccagcttttg ttccctttag tgagggttaa ttgcgcgctt ggcgtaatca   3240
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gccggaagca taaagtgtaa agcctggggt gcctaatgag tgagctaact cacattaatt   3360
gcgttgcgct cactgcccgc tttccagtcg ggaaacctgt cgtgccagct gcattaatga   3420
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cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc   3660
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aacccggtaa gacacgactt atcgccactg gcagcagcca ctggtaacag gattagcaga   4020
gcgaggtatg taggcggtgc tacagagttc ttgaagtggt ggcctaacta cggctacact   4080
agaaggacag tatttggtat ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt   4140
ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtggtttttt tgtttgcaag   4200
cagcagatta cgcgcagaaa aaaaggatct caagaagatc ctttgatctt ttctacgggg   4260
tctgacgctc agtggaacga aaactcacgt taagggattt tggtcatgag attatcaaaa   4320
```

9

```
aggatcttca cctagatcct tttaaattaa aaatgaagtt ttaaatcaat ctaaagtata    4380
tatgagtaaa cttggtctga cagttaccaa tgcttaatca gtgaggcacc tatctcagcg    4440
atctgtctat ttcgttcatc catagttgcc tgactccccg tcgtgtagat aactacgata    4500
cgggagggct taccatctgg ccccagtgct gcaatgatac cgcgagaccc acgctcaccg    4560
gctccagatt tatcagcaat aaaccagcca gccggaaggg ccgagcgcag aagtggtcct    4620
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tagtgtatgc ggcgaccgag ttgctcttgc ccggcgtcaa tacgggataa taccgcgcca    5040
catagcagaa ctttaaaagt gctcatcatt ggaaaacgtt cttcggggcg aaaactctca    5100
aggatcttac cgctgttgag atccagttcg atgtaaccca ctcgtgcacc caactgatct    5160
tcagcatctt ttactttcac cagcgtttct gggtgagcaa aaacaggaag gcaaaatgcc    5220
gcaaaaaagg gaataagggc gacacggaaa tgttgaatac tcatactctt ccttttttcaa    5280
tattattgaa gcatttatca gggttattgt ctcatgagcg gatacatatt tgaatgtatt    5340
tagaaaaata aacaaatagg ggttccgcgc acatttcccc gaaaagtgcc ac            5392
```

<210> 7
<211> 5173
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene from Hordeum vulgare from nucleotide 2199 to
      nucleotide 2450 in a Zea mays expression vector.
      Zea mays promoter from nucleotide 676 to
      nucleotide 2198.

<400> 7

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ctaaattgta agcgttaata ttttgttaaa attcgcgtta aattttttgtt aaatcagctc      60
atttttttaac caataggccg aaatcggcaa aatcccttat aaatcaaaag aatagaccga     120
gatagggttg agtgttgttc cagtttggaa caagagtcca ctattaaaga acgtggactc     180
caacgtcaaa gggcgaaaaa ccgtctatca gggcgatggc ccactacgtg aaccatcacc     240
ctaatcaagt tttttggggt cgaggtgccg taaagcacta aatcggaacc ctaaagggag     300
cccccgattt agagcttgac ggggaaagcc ggcgaacgtg gcgagaaagg aagggaagaa     360
agcgaaagga gcgggcgcta gggcgctggc aagtgtagcg gtcacgctgc gcgtaaccac     420
cacacccgcc gcgcttaatg cgccgctaca gggcgcgtcc cattcgccat tcaggctgcg     480
caactgttgg gaagggcgat cggtgcgggc ctcttcgcta ttacgccagc tggcgaaagg     540
gggatgtgct gcaaggcgat taagttgggt aacgccaggg ttttcccagt cacgacgttg     600
taaaacgacg gccagtgagc gcgcgtaata cgactcacta tagggcgaat tggagctcca     660
ccgcggtggc ggccgctcta gattatataa tttataagct aaacaacccg gccctaaagc     720
actatcgtat cacctatcta aataagtcac gggagtttcg aacgtccact tcgtcgcacg     780
gaattgcatg tttcttgttg gaagcatatt cacgcaatct ccacacataa aggtttatgt     840
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caatccatat aagttagagt aaaaaataag tttaaatttt atcttaattc actccaacat     960
atatggatct acaatactca tgtgcatcca aacaaactac ttatattgag gtgaatttgg    1020
tagaaattaa actaacttac acactaagcc aatctttact atattaaagc accagtttca    1080
acgatcgtcc cgcgtcaata ttattaaaaa actcctacat ttctttataa tcaacccgca    1140
ctcttataat ctcttctcta ctactataat aagagagttt atgtacaaaa taaggtgaaa    1200
ttatctataa gtgttctgga tattggttgt tggctcccat attcacacaa cctaatcaat    1260
agaaaacata tgtttttatta aaacaaaatt tatcatatat catatatata tatatatcat    1320
atatatatat aaaccgtagc aatgcacggg catataacta gtgcaactta atacatgtgt    1380
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gaggaacacg aaagaaccat gcattggcat gtaaagctcc aagaatttgt tgtatcctta    1620
acaactcaca gaacatcaac caaaattgca cgtcaagggt attgggtaag aaacaatcaa    1680
acaaatcctc tctgtgtgca aagaaacacg gtgagtcatg ccgagatcat actcatctga    1740
```

10

```
tatacatgct tacagctcac aagacattac aaacaactca tattgcatta caaagatcgt    1800
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caacaaaaaa aaagccatat gtcaagctaa atctaattcg ttttacgtag atcaacaacc    1920
tgtagaaggc aacaaaactg agccacgcag aagtacagaa tgattccaga tgaaccatcg    1980
acgtgctacg taaagagagt gacgagtcat atacatttgg caagaaacca tgaagctgcc    2040
tacagccgta tcggtggcat aagaacacaa gaaattgtgt taattaatca aagctataaa    2100
taacgctcgc atgcctgtgc acttctccat caccaccact gggtcttcag accattagct    2160
ttatctactc cagagcgcag aagaacccga tcgacaccat gaagtcggtg gagaagaaac    2220
cgaagggtgt gaagacaggt gcgggtgaca agcataagct gaagacagag tggccggagt    2280
tggtggggaa atcggtggag aaagccaaga aggtgatcct gaaggacaag ccagaggcgc    2340
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ctcatactct tcctttttca atattattga agcatttatc agggttattg tctcatgagc    5100
ggatacatat ttgaatgtat ttagaaaaat aaacaaatag gggttccgcg cacatttccc    5160
cgaaaagtgc cac                                                       5173
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11

<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer designed based upon the alpha hordothionin
     sequence from Hordeum vulgare to amplify the gene
     and to introduce a NcoI site at the start (ATG)
     codon and a BamHI site after the stop codon of the
     thionin coding sequence to facilitate cloning.

<400> 8
agtataagta aacacaccat cacacccttg aggcccttgc tggtggccat ggtg   54

<210> 9
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer designed based upon the alpha hordothionin
     sequence of Hordeum vulgare to amplify the gene
     and to introduce a NcoI site at the start (ATG)
     codon and a BamHI site after the stop codon of the
     thionin coding sequence to facilitate cloning.

<400> 9
cctcacatcc cttagtgcct aagttcgacg tcgggccctc tagtcgacgg atcca   55

<210> 10
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer designed for single stranded DNA
     site-directed mutagenesis to introduce into the
     native Hordeum vulgare alpha hordothionin gene 12
     codons for lysine, based on the peptide structure
     of hordothionin 12.

<400> 10
agcggaaaat gcccgaaagg cttccccaaa ttggc   35

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer designed for single stranded DNA
     site-directed mutagenesis to introduce into the
     native Hordeum vulgare alpha hordothionin gene 12
     codons for lysine, based on the peptide structure
     of hordothionin 12.

<400> 11
tgcgcaggcg tctgcaagtg taagctgact agtagcggaa aatgc   45

<210> 12
<211> 50

<210> DNA
<213> Artificial Sequence

<220>
<223> Primer designed for single stranded DNA
      site-directed mutagenesis to introduce into the
      native Hordeum vulgare alpha hordothionin gene 12
      codons for lysine, based on the peptide structure
      of hordothionin 12.

<400> 12
tacaaccttt gcaaagtcaa aggcgccaag aagctttgcg caggcgtctg   50

<210> 13
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer designed for single stranded DNA
      site-directed mutagenesis to introduce into the
      native Hordeum vulgare alpha hordothionin gene 12
      codons for lysine, based on the peptide structure
      of hordothionin 12.

<400> 13
gcaagagttg ctgcaagagt accctgggaa ggaagtgcta caacctttgc   50

<210> 14
<211> 609
<212> DNA
<213> Pisum sativum

<220>
<221> CDS
<222> (18)...(410)

<400> 14

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tttctttcta tcaaaca atg gct tcc gtt aaa ctc gct tct ttg atg gtc          50
                    Met Ala Ser Val Lys Leu Ala Ser Leu Met Val
                     1               5                       10

ttg ttt gcc aca tta ggt atg ttc ctg aca aaa aac gta gga gca gca          98
Leu Phe Ala Thr Leu Gly Met Phe Leu Thr Lys Asn Val Gly Ala Ala
             15                  20                  25

agc tgc aat ggg gtt tgt tct cca ttt gag atg cca cca tgt ggc tct         146
Ser Cys Asn Gly Val Cys Ser Pro Phe Glu Met Pro Pro Cys Gly Ser
         30                  35                  40

tca gcc tgt cga tgt atc cct gtt ggt cta gtt gtt ggt tac tgc aga         194
Ser Ala Cys Arg Cys Ile Pro Val Gly Leu Val Val Gly Tyr Cys Arg
     45                  50                  55

cat cca tct gga gtt ttc ttg agg acg aat gat gaa cac cct aac tta         242
His Pro Ser Gly Val Phe Leu Arg Thr Asn Asp Glu His Pro Asn Leu
 60                  65                  70                  75

tgt gag tct gat gcc gat tgt agg aag aaa gga agt ggt aac ttt tgc         290
Cys Glu Ser Asp Ala Asp Cys Arg Lys Lys Gly Ser Gly Asn Phe Cys
                 80                  85                  90
```

13

```
ggt cat tat cct aat cct gat att gaa tat gga tgg tgt ttt gcc tct      338
Gly His Tyr Pro Asn Pro Asp Ile Glu Tyr Gly Trp Cys Phe Ala Ser
            95                  100                 105

aaa tct gaa gca gaa gac ttt ttc tct aag att acc caa aaa gac ttg      386
Lys Ser Glu Ala Glu Asp Phe Phe Ser Lys Ile Thr Gln Lys Asp Leu
            110                 115                 120

ttg aag agt gtt tcc act gct taa tttccatatc cagaacaaaa ccatgcatgc    440
Leu Lys Ser Val Ser Thr Ala *
            125                 130

aagacatggt gaagctatct agtactttaa ataaacaaac tttgtttcca acataggagt    500
tggatttcta agatacgcat cacaattcca ataaatgtta tatgtgcatg gttccagtgt    560
tgtaatatat gcagtttctt ttcaaataat aaatcttata tcacaattg               609


        <210> 15
        <211> 130
        <212> PRT
        <213> Pisum sativum

        <400> 15
Met Ala Ser Val Lys Leu Ala Ser Leu Met Val Leu Phe Ala Thr Leu
1               5                   10                  15
Gly Met Phe Leu Thr Lys Asn Val Gly Ala Ala Ser Cys Asn Gly Val
            20                  25                  30
Cys Ser Pro Phe Glu Met Pro Pro Cys Gly Ser Ser Ala Cys Arg Cys
            35                  40                  45
Ile Pro Val Gly Leu Val Val Gly Tyr Cys Arg His Pro Ser Gly Val
            50                  55                  60
Phe Leu Arg Thr Asn Asp Glu His Pro Asn Leu Cys Glu Ser Asp Ala
65                  70                  75                  80
Asp Cys Arg Lys Lys Gly Ser Gly Asn Phe Cys Gly His Tyr Pro Asn
            85                  90                  95
Pro Asp Ile Glu Tyr Gly Trp Cys Phe Ala Ser Lys Ser Glu Ala Glu
            100                 105                 110
Asp Phe Phe Ser Lys Ile Thr Gln Lys Asp Leu Leu Lys Ser Val Ser
            115                 120                 125
Thr Ala
    130


        <210> 16
        <211> 1240
        <212> DNA
        <213> Zea mays

        <220>
        <221> CDS
        <222> (234)...(776)

        <400> 16
gaattcattg acaacccttg acatgtaaag ttgattcata tgtataagaa agcttaatga     60
tctatctgta catccaaatc catgtactat gtttccacgt catgcaacgc aacattccaa    120
aaccatggat catctataaa tggctagctc ccacatatga actagtctct atcatcatcc    180
aatccagatc agcaaagcgg cagtgcgtag agaggatcgt cgaacagaac agc atg       236
                                                              Met
                                                              1

aag atg gtc atc gtt ctc gtc gtg tgc ctg gct ctg tca gct gcc tgc     284
Lys Met Val Ile Val Leu Val Val Cys Leu Ala Leu Ser Ala Ala Cys
            5                   10                  15
```

14

```
gcc tct gca atg cag atg ccc tgc ccc tgc gcg ggg ctg cag ggc ttg        332
Ala Ser Ala Met Gln Met Pro Cys Pro Cys Ala Gly Leu Gln Gly Leu
         20                  25                  30

tac ggc gct ggc gcc ggc ctg acg acg atg atg ggc gcc ggc ggg ctg        380
Tyr Gly Ala Gly Ala Gly Leu Thr Thr Met Met Gly Ala Gly Gly Leu
         35                  40                  45

tac ccc tac gcg gag tac ctg agg cag ccg cag tgc agc ccg ctg gcg        428
Tyr Pro Tyr Ala Glu Tyr Leu Arg Gln Pro Gln Cys Ser Pro Leu Ala
50                  55                  60                  65

gcg gcg ccc tac tac gcc ggg tgt ggg cag acg agc gcc atg tac cag        476
Ala Ala Pro Tyr Tyr Ala Gly Cys Gly Gln Thr Ser Ala Met Tyr Gln
                70                  75                  80

ccg ctc cgg caa cag tgc tgc cag cag cag atg agg atg atg gac gtg        524
Pro Leu Arg Gln Gln Cys Cys Gln Gln Gln Met Arg Met Met Asp Val
                85                  90                  95

cag tcc gtc gcg cag cag ctg cag atg atg atg cag ctt gag cgt gcc        572
Gln Ser Val Ala Gln Gln Leu Gln Met Met Met Gln Leu Glu Arg Ala
         100                 105                 110

gct gcc gcc agc agc agc ctg tac gag cca gct ctg atg cag cag cag        620
Ala Ala Ala Ser Ser Ser Leu Tyr Glu Pro Ala Leu Met Gln Gln Gln
         115                 120                 125

cag cag ctg ctg gca gtc cag ggt ctc aac ccc atg gcc atg atg atg        668
Gln Gln Leu Leu Ala Val Gln Gly Leu Asn Pro Met Ala Met Met Met
130                 135                 140                 145

gcg cag aac atg ccg gcc atg ggt gga ctc tac cag tac cag tac cag        716
Ala Gln Asn Met Pro Ala Met Gly Gly Leu Tyr Gln Tyr Gln Tyr Gln
                150                 155                 160

ctg ccc agc tac cgc acc aac ccc tgt ggc gtc tcc gct gcc att ccg        764
Leu Pro Ser Tyr Arg Thr Asn Pro Cys Gly Val Ser Ala Ala Ile Pro
                165                 170                 175

ccc tac tac tga ttcatgatat ttgggaaatc tcctctatcc atccctctct          816
Pro Tyr Tyr  *
         180

atctatatat gtaataatgc agtaagacga cacacattat catgtgtggt atgaccaata    876
atatatgcat cataataaag ttttggtttt aaagaattat cggacgcttg atatctatga    936
tgctggataa atcaaaactt ctcatataaa ttgtaaatat ttcaaaatct ctatttaggc    996
tccaatggag agcatatggg tagagtagta tatatgcttg aaatactaac aactagcaaa   1056
gtgcgggcac gttgctacat gctcatttat gctcgagcat ggagtataaa acataaagat   1116
atatatgttc cattggcctg gtaaacgctg gatataggtt taaagccaac aactcatggt   1176
tcgaatcccc atttatatat aatccataat tttagcgctt tttaccattt aaatttggga   1236
gtaa                                                                1240
```

```
        <210> 17
        <211> 180
        <212> PRT
        <213> Zea mays

        <400> 17
Met Lys Met Val Ile Val Leu Val Val Cys Leu Ala Leu Ser Ala Ala
1               5                   10                  15
Cys Ala Ser Ala Met Gln Met Pro Cys Pro Cys Ala Gly Leu Gln Gly
```

15

```
                    20                      25                      30
Leu Tyr Gly Ala Gly Ala Gly Leu Thr Thr Met Met Gly Ala Gly Gly
            35                      40                      45
Leu Tyr Pro Tyr Ala Glu Tyr Leu Arg Gln Pro Gln Cys Ser Pro Leu
        50                      55                      60
Ala Ala Ala Pro Tyr Tyr Ala Gly Cys Gly Gln Thr Ser Ala Met Tyr
65                      70                      75                      80
Gln Pro Leu Arg Gln Gln Cys Cys Gln Gln Gln Met Arg Met Met Asp
                85                      90                      95
Val Gln Ser Val Ala Gln Gln Leu Gln Met Met Met Gln Leu Glu Arg
               100                     105                     110
Ala Ala Ala Ala Ser Ser Ser Leu Tyr Glu Pro Ala Leu Met Gln Gln
               115                     120                     125
Gln Gln Gln Leu Leu Ala Val Gln Gly Leu Asn Pro Met Ala Met Met
       130                     135                     140
Met Ala Gln Asn Met Pro Ala Met Gly Gly Leu Tyr Gln Tyr Gln Tyr
145                     150                     155                     160
Gln Leu Pro Ser Tyr Arg Thr Asn Pro Cys Gly Val Ser Ala Ala Ile
                       165                     170                     175
Pro Pro Tyr Tyr
            180


        <210> 18
        <211> 2562
        <212> DNA
        <213> Zea mays

        <220>
        <221> CDS
        <222> (1137)...(1589)

        <400> 18
aagcttgcta ctttctttcc ttaatgttga tttccccttt gttagatgtt ctttgtgtta     60
tatacactct gtatacaagg atgcgataca cacatcagct agtcctaatg atgccaccga    120
ctttacttga ggaaaaggaa acaaatatga tgtggccatc acattctcaa taacaatgac    180
catgtgcgca atgacatacc atcatatttg atatcataaa aataaattta ttatcaaagt    240
aaacatatag ttcatatatc agatattaaa gtgataagaa caaatattac attttatctt    300
atataaaatg acgaaaaagg tacgagttga aaaggagtcc aacccctttt ttatagcttg    360
ttcggttgct tgttctcttc ggctagcgag gtggtagaat gtgagagtgt tgcgcgtgga    420
ttcccgtcgt agtgttctta ggtgatttct cacggcccat ctgtgatata gcgactcata    480
tgtggtgtaa tagcccattg ggagaagggg agagatatag atctacgtga tttgcacgtg    540
atgcacgacg aacgaaactg gtggtttaaa gtagtagagg tttgtcatta gaggtgtaaa    600
tggtacatat attatccgtt catattcgaa tttgatccgt ataagagggc taagatctaa    660
tccgtataca agtccaagta ttaagtatcc gatccatatc ggatctttat ccgtatccgt    720
atactcaaaa tttgatgttt aagattttaa tatatattta aactttatag gaactcgata    780
atatttgtat ctgatttgaa ttatgaaaac aaatatggaa cgattaattt cagtctatat    840
ccgttccgat atttgtcatg ctttgctaaa aataccttta caaggcatct tgtgcagatt    900
atatattaat ctgaaatcag ttagagaagc ctacaaattt gaccaaatgc cgagtcatcc    960
ggcttatccc ctttccaact ttcagttctg caagcgccag aaatcgtttt tcatctacat   1020
tgtctttgtt gcctgcatac atctataaat aggacctgct agatcaatcg cagtccatcg   1080
gcctcagtcg cacatatcta ctatactata ctctaggaag caaggacacc accgcc atg   1139
                                                                  Met
                                                                    1


gca gcc aag atg ctt gca ttg ttc gct ctc cta gct ctt tgt gca agc   1187
Ala Ala Lys Met Leu Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala Ser
              5                      10                      15


gcc act agt gcg acc cat att cca ggg cac ttg cca cca gtc atg cca   1235
Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Pro Pro Val Met Pro
            20                      25                      30
```

16

```
ttg ggt acc atg aac cca tgc atg cag tac tgc atg atg caa cag ggg    1283
Leu Gly Thr Met Asn Pro Cys Met Gln Tyr Cys Met Met Gln Gln Gly
    35              40                  45

ctt gcc agc ttg atg gcg tgt ccg tcc ctg atg ctg cag caa ctg ttg    1331
Leu Ala Ser Leu Met Ala Cys Pro Ser Leu Met Leu Gln Gln Leu Leu
50                  55                  60                  65

gcc tta ccg ctt cag acg atg cca gtg atg atg cca cag atg atg acg    1379
Ala Leu Pro Leu Gln Thr Met Pro Val Met Met Pro Gln Met Met Thr
            70                  75                  80

cct aac atg atg tca cca ttg atg atg ccg agc atg atg tca cca atg    1427
Pro Asn Met Met Ser Pro Leu Met Met Pro Ser Met Met Ser Pro Met
            85                  90                  95

gtc ttg ccg agc atg atg tcg caa ata atg atg cca caa tgt cac tgc    1475
Val Leu Pro Ser Met Met Ser Gln Ile Met Met Pro Gln Cys His Cys
        100                 105                 110

gac gcc gtc tcg cag att atg ctg caa cag cag tta cca ttc atg ttc    1523
Asp Ala Val Ser Gln Ile Met Leu Gln Gln Gln Leu Pro Phe Met Phe
        115                 120                 125

aac cca atg gcc atg acg att cca ccc atg ttc tta cag caa ccc ttt    1571
Asn Pro Met Ala Met Thr Ile Pro Pro Met Phe Leu Gln Gln Pro Phe
130                 135                 140                 145

gtt ggt gct gca ttc tag atagaaatat ttgtgttgta tcgaataatg          1619
Val Gly Ala Ala Phe  *
                150

agttgacatg ccatcgcgtg tgactcatta ttaacaataa aacaagtttc ctcttattat    1679
cttttatat ctctccctat ccattttgc aaagcccatt atcctttact ccctaagtcc     1739
caatatattt tagaccttaa attgtatgtc tatattcaaa agaatgacaa taaatctaga    1799
catatatata aaacacatac attaagtatt gtatgaatct attaaaatgc taaaacgact    1859
aatattatgg gacggaggga gtactttatt agtagattac attgttattt tctctattcc    1919
aaatataagt ctggttttc aatcaatcaa tatatattac catgtccaaa cattttgaat     1979
tatatatcta ggtgcagcat ccgtgcacga tcgtaaaaga agcagtcacg gtgttggtcc    2039
caaaaactaa tcgtccgttg tcggtcacct ataaagattc atgaagagaa ccaaaataag    2099
gcaatataat taatgtaata tgactcctcc ttttgaatta cttaggaata acataagcaa    2159
acaaaaaaag gagaagatca aggtaaataa aggcattttg tgagaaaaca tggaagcata    2219
agaatgcata agtaatgatt tgtgtctctt tatatttttt ttattcacgt gaatttacat    2279
agataccatc ggatgttcga tggtaataca atgatgcctt agctccgaga gcttcgaatg    2339
atgagcgatt taaaaatact cctatcaatt gttcgaaagt tctttgtctc atgcatgggc    2399
aatgtacctc tatttatagg gacggtgcga cgtacaaatt tgtataaaat tatatttta    2459
ttcccaaatc ctatgcatat gtgtcgggga ccataattag gggtaccctc aaggctccta    2519
attctcagct ggtaaccccca tcagcataaa gctgcaaagg cct                    2562

        <210> 19
        <211> 150
        <212> PRT
        <213> Zea mays

        <400> 19
Met Ala Ala Lys Met Leu Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
1               5                   10                  15
Ser Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Pro Pro Val Met
            20                  25                  30
Pro Leu Gly Thr Met Asn Pro Cys Met Gln Tyr Cys Met Met Gln Gln
        35                  40                  45
Gly Leu Ala Ser Leu Met Ala Cys Pro Ser Leu Met Leu Gln Gln Leu
```

17

```
        50                      55                      60
Leu Ala Leu Pro Leu Gln Thr Met Pro Val Met Met Pro Gln Met Met
65                      70                      75                      80
Thr Pro Asn Met Met Ser Pro Leu Met Met Pro Ser Met Met Ser Pro
                    85                      90                      95
Met Val Leu Pro Ser Met Met Ser Gln Ile Met Met Pro Gln Cys His
                    100                     105                     110
Cys Asp Ala Val Ser Gln Ile Met Leu Gln Gln Gln Leu Pro Phe Met
        115                     120                     125
Phe Asn Pro Met Ala Met Thr Ile Pro Pro Met Phe Leu Gln Gln Pro
    130                     135                     140
Phe Val Gly Ala Ala Phe
145                     150
```

<210> 20
<211> 562
<212> DNA
<213> Oryza sativa

<220>
<221> CDS
<222> (51)...(455)

<400> 20

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cgtctacacc atctggaatc ttgtttaaca ctagtattgt agaatcagca atg gca        56
                                                        Met Ala
                                                        1

gca tac acc agc aag atc ttt gcc ctg ttt gcc tta att gct ctt tct      104
Ala Tyr Thr Ser Lys Ile Phe Ala Leu Phe Ala Leu Ile Ala Leu Ser
            5                   10                  15

gca agt gcc act act gca atc acc act atg cag tat ttc cca cca aca      152
Ala Ser Ala Thr Thr Ala Ile Thr Thr Met Gln Tyr Phe Pro Pro Thr
    20                  25                  30

tta gcc atg ggc acc atg gat ccg tgt agg cag tac atg atg caa acg      200
Leu Ala Met Gly Thr Met Asp Pro Cys Arg Gln Tyr Met Met Gln Thr
35                  40                  45                  50

ttg ggc atg ggt agc tcc aca gcc atg ttc atg tcg cag cca atg gcg      248
Leu Gly Met Gly Ser Ser Thr Ala Met Phe Met Ser Gln Pro Met Ala
                    55                  60                  65

ctc ctg cag cag caa tgt tgc atg cag cta caa ggc atg atg cct cag      296
Leu Leu Gln Gln Gln Cys Cys Met Gln Leu Gln Gly Met Met Pro Gln
                70                  75                  80

tgc cac tgt ggc acc agt tgc cag atg atg cag agc atg caa caa gtt      344
Cys His Cys Gly Thr Ser Cys Gln Met Met Gln Ser Met Gln Gln Val
                85                  90                  95

att tgt gct gga ctc ggg cag cag cag atg atg aag atg gcg atg cag      392
Ile Cys Ala Gly Leu Gly Gln Gln Gln Met Met Lys Met Ala Met Gln
    100                 105                 110

atg cca tac atg tgc aac atg gcc cct gtc aac ttc caa ctc tct tcc      440
Met Pro Tyr Met Cys Asn Met Ala Pro Val Asn Phe Gln Leu Ser Ser
115                 120                 125                 130

tgt ggt tgt tgt tga tcaaacgttg gttacatgta ctctagtaat aaggtgttgc      495
Cys Gly Cys Cys  *
```

18

```
atactatcgt gtgcaaacac tagaaataag aaccattgaa taaaatatca atcattttca    555
gacttgc                                                              562
```

<210> 21
<211> 134
<212> PRT
<213> Oryza sativa

<400> 21

```
Met Ala Ala Tyr Thr Ser Lys Ile Phe Ala Leu Phe Ala Leu Ile Ala
1               5                   10                  15
Leu Ser Ala Ser Ala Thr Thr Ala Ile Thr Thr Met Gln Tyr Phe Pro
            20                  25                  30
Pro Thr Leu Ala Met Gly Thr Met Asp Pro Cys Arg Gln Tyr Met Met
            35                  40                  45
Gln Thr Leu Gly Met Gly Ser Ser Thr Ala Met Phe Met Ser Gln Pro
        50                  55                  60
Met Ala Leu Leu Gln Gln Gln Cys Cys Met Gln Leu Gln Gly Met Met
65                  70                  75                      80
Pro Gln Cys His Cys Gly Thr Ser Cys Gln Met Met Gln Ser Met Gln
                85                  90                  95
Gln Val Ile Cys Ala Gly Leu Gly Gln Gln Gln Met Met Lys Met Ala
            100                 105                 110
Met Gln Met Pro Tyr Met Cys Asn Met Ala Pro Val Asn Phe Gln Leu
            115                 120                 125
Ser Ser Cys Gly Cys Cys
130
```

<210> 22
<211> 45
<212> PRT
<213> Triticum aestivum

<400> 22

```
Lys Ser Cys Cys Lys Ser Thr Leu Gly Arg Asn Cys Tyr Asn Leu Cys
1               5                   10                  15
Arg Ala Arg Gly Ala Gln Lys Leu Cys Ala Asn Val Cys Arg Cys Lys
            20                  25                  30
Leu Thr Ser Gly Leu Ser Cys Pro Lys Asp Phe Pro Lys
            35                  40                  45
```